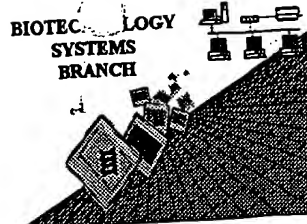


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/623,514
Source: Pg/09
Date Processed by STIC: 4/25/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

SERIAL NUMBER: 09/623,514

ERROR DETECTED SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of "Artificial" (NEW RULES)

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 _____ Use of <220>Feature (NEW RULES)

Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/623,514

DATE: 04/25/2001
TIME: 08:43:04

Input Set : A:\43922.txt
Output Set: N:\CRF3\04252001\I623514.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: National Research Council of Canada
4 Zou, Jitao
5 Taylor, David C
6 Wei, Yangdou
7 Jako, Colette C
9 <120> TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants
11 <130> FILE REFERENCE: 43922pt
13 <140> CURRENT APPLICATION NUMBER: US/09/623,514
14 <141> CURRENT FILING DATE: 2000-10-02
16 <150> PRIOR APPLICATION NUMBER: 60/112,812
17 <151> PRIOR FILING DATE: 1998-12-17
19 <160> NUMBER OF SEQ ID NOS: 25
21 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

470 <210> SEQ ID NO: 6
471 <211> LENGTH: 629
472 <212> TYPE: DNA
473 <213> ORGANISM: Arabidopsis thaliana
475 <400> SEQUENCE: 6
476 tgcattgtata cggaagggtt ggggtggtcg tcaatttgca aaactgggtca tattcaccgg 60
477 attcatggga ttataatag aacaatatat aaatcctatt gtcaggaact caaagcatcc 120
478 ttgaaaggc gatcttctat atgctattga aagagtgttg aagctttcag ttccaaattt 180
479 atatgtgtgg ctctgcatgt tctactgctt cttccacctt tggttaaaca tattggcaga 240
480 gcttctctgc ttcggggatc gtgaattcta caaagattgg tggaaatgcaa aaagtgtggg 300
481 agattactgg gagaatgtgg aatatgcctg tccataaatg ggatgggtcc gacatatata 360
482 ccttccccgt gcttgcgcac aaggattacc caaagacacc ccggccatta accattgggt 420
E--> 483 ttcccaagcc ccctggaggc ctttccatgg gccanggacc cggngtncce tggdnggccc 480
E--> 484 ttcaaagcaa agggggnttn cctggggnta aagntccang ggcccttggg gcccangcaa 540
E--> 485 aannttcccc cgggaaaggg ttgcccaccg gggggngaaa aanncccggg ggcacnccgg 600
486 aattttggga acccgggggg ggccttttt 629

see
item 10
on Error
summary
sheet

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/623,514

DATE: 04/25/2001

TIME: 08:43:05

Input Set : A:\43922.txt

Output Set: N:\CRF3\04252001\I623514.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:483 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
M:340 Repeated in SeqNo=6
L:700 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10